

RECEIVED

JUN 01 2001

TECH CENTER 1600/2900

1

SEQUENCE LISTING

1510

<110> ZIMMET, PAUL Z.
COLLIER, GREGORY

<120> A NOVEL GENE AND USES THEREFOR

<130> 22975-20007.00

<140> 09/331,930
<141> 1999-06-30

<150> PCT/AU98/00902
<151> 1998-10-30

<150> AU PP0117/97
<151> 1997-10-31

<150> AU PP0323/97
<151> 1997-11-11

<160> 27

<170> PatentIn Ver. 2.1

Q1
<210> 1
<211> 342
<212> DNA
<213> Unknown Organism

<220>

<223> Description of Unknown Organism: DNA sequence for
beacon from unknown organism

<220>

<221> CDS
<222> (29) .. (247)

<400> 1

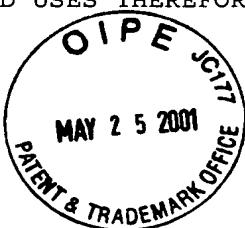
gttccaggag attacagctc cagccaca atg att gag gtg gtt tgc aac gac 52
Met Ile Glu Val Val Cys Asn Asp
1 5

cgt cta gga aag aaa gtc cgc gtt aag tgc aac acc gat gac acc atc 100
Arg Leu Gly Lys Lys Val Arg Val Lys Cys Asn Thr Asp Asp Thr Ile
10 15 20

ggg gac ttg aag aaa ctg ata gcg gcc caa act ggc act cgt tgg aat 148
Gly Asp Leu Lys Lys Leu Ile Ala Ala Gln Thr Gly Thr Arg Trp Asn
25 30 35 40

aag atc gtt ctt aaa aag tgg tac acg att ttt aag gac cat gta tct 196
Lys Ile Val Leu Lys Trp Tyr Thr Ile Phe Lys Asp His Val Ser
45 50 55

ctg gga gat tat gaa atc cac gat ggg atg aac ctg gag ctt tat tac 244
Leu Gly Asp Tyr Glu Ile His Asp Gly Met Asn Leu Glu Leu Tyr Tyr
60 65 70



51

A

cag tagagggaa ttcctccacc ttgcccacc ttgccttcct ctccccatggc 297
 Gln

tcatttaaca ctgtttaga tgctcatttt tttgttaagt gtact 342

<210> 2
 <211> 73
 <212> PRT
 <213> Unknown Organism

<220>
 <223> Description of Unknown Organism: Amino acid sequence for beacon from unknown organism

<400> 2
 Met Ile Glu Val Val Cys Asn Asp Arg Leu Gly Lys Lys Val Arg Val
 1 5 10 15

Lys Cys Asn Thr Asp Asp Thr Ile Gly Asp Leu Lys Lys Leu Ile Ala
 20 25 30

Ala Gln Thr Gly Thr Arg Trp Asn Lys Ile Val Leu Lys Lys Trp Tyr
 35 40 45

Thr Ile Phe Lys Asp His Val Ser Leu Gly Asp Tyr Glu Ile His Asp
 50 55 60

Gly Met Asn Leu Glu Leu Tyr Tyr Gln
 65 70

<210> 3
 <211> 391
 <212> DNA
 <213> Unknown Organism

<220>
 <223> Description of Unknown Organism: Complimentary sequence for SEQ ID NO: 1

<400> 3
 atgttcaaca cagcagccat ccaaggcct ctaatgtcga ggtcggtgtt actaactcca 60
 ccaaacgttg ctggcagatc ctttcttca ggcgaattc acgttgtggc tactgtggta 120
 gcccctgaac ttctttgact atcgccgggt ttgaccgtga gcaaccttat tctagcaaga 180
 atttttcacc atgtgctaaa aattcctggt acatagagac cctctaatac tttaggtgct 240
 accctacttg gacctcgaaa taatggtcat ctcccccttaa ggaggtggaa cgggttggaa 300
 ccaaaggaga gggtaccgag taaattgtga caacatctac gagaaaaaaaaa acaattcaca 360
 tgaataaaaaa ctttgatgct gcaaaaaaaaaa a 391

<210> 4
 <211> 16
 <212> DNA
 <213> Artificial Sequence

52

A

<220>
<223> Description of Artificial Sequence: Primer

<400> 4
aagctttttt ttttg

16

<210> 5
<211> 13
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 5
aagcttcggg taa

13

<210> 6
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 6
agtccgcgtt aagtgcaca

20

<210> 7
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 7
ctccagggtc atccccatcg

20

<210> 8
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 8
ggctacagct tcaccaccac

20

<210> 9
<211> 20
<212> DNA

53

8

<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 9
gcttgctgat ccacatctgc 20

<210> 10
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Probe
'
<400> 10
tggtaataaaa gctccagggtt catcccatcg 30

<210> 11
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 11
caaactggca ctcgttggaa 20

<210> 12
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 12
gttgggcaag gtggaggaa 19

<210> 13
<211> 102
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)..(99)

<220>
<221> modified_base
<222> (44)
<223> a, t, c or g

54 A

<400> 13
atg atc gag gtt gtt tgc aac gac cgt ctg ggg aaa aag gtc cnc gtt 48
Met Ile Glu Val Val Cys Asn Asp Arg Leu Gly Lys Lys Val Xaa Val
1 5 10 15

aaa tgc aac acg gat gat acc atc ggg gac ctt aag aag ctg att gca 96
Lys Cys Asn Thr Asp Asp Thr Ile Gly Asp Leu Lys Lys Leu Ile Ala
20 25 30

gcc taa 102
Ala

<210> 14
<211> 33
<212> PRT
<213> Homo sapiens

<220>
<221> MOD_RES
<222> (15)
<223> variable amino acid

<400> 14
Met Ile Glu Val Val Cys Asn Asp Arg Leu Gly Lys Lys Val Xaa Val 48
1 5 10 15

Lys Cys Asn Thr Asp Asp Thr Ile Gly Asp Leu Lys Lys Leu Ile Ala
20 25 30

Ala

<210> 15
<211> 222
<212> DNA
<213> Psammomys obesus

<220>
<221> CDS
<222> (1)..(99)

<400> 15
aag atc gtt ctt aaa aag tgg tac acg att ttt aag gac cat gta tct 48
Lys Ile Val Leu Lys Lys Trp Tyr Thr Ile Phe Lys Asp His Val Ser
1 5 10 15

ctg gga gat tat gaa atc cac gat ggg atg aac ctg gag ctt tat tac 96
Leu Gly Asp Tyr Glu Ile His Asp Gly Met Asn Leu Glu Leu Tyr Tyr
20 25 30

cag tagagggaa ttccctccacc ttgccccacc ttgccttcct ctcccatggc 149
Gln

tcatttaaca ctgtttaga tgctcatttt taacaattca catgaataaa aactttgatg 209

55

8

ctgaaaaaaaaaaa

222

<210> 16
<211> 33
<212> PRT
<213> Psammomys obesus

<400> 16
Lys Ile Val Leu Lys Lys Trp Tyr Thr Ile Phe Lys Asp His Val Ser
1 5 10 15
Leu Gly Asp Tyr Glu Ile His Asp Gly Met Asn Leu Glu Leu Tyr Tyr
20 25 30

Gln

<210> 17
<211> 222
<212> DNA
<213> Psammomys obesus

<220>
<221> CDS
<222> (1)..(99)

<400> 17
aag atc gtt ctt aaa aag tgg tac acg att ttt aag gac cat gta tct 48
Lys Ile Val Leu Lys Lys Trp Tyr Thr Ile Phe Lys Asp His Val Ser
1 5 10 15

ctg gga gat tat gaa atc cac gat ggg atg aac ctg gag ctt tat tac 96
Leu Gly Asp Tyr Glu Ile His Asp Gly Met Asn Leu Glu Leu Tyr Tyr
20 25 30

cag tagagggaa ttccctccacc ttgccccacc ttgcttcct ctcccatggc 149
Gln

tcatttaaca ctgttgtaga tgctcatttt taacaattca catgaataaa aactttgatg 209

ctgaaaaaaaaaaa 222

<210> 18
<211> 33
<212> PRT
<213> Psammomys obesus

<400> 18
Lys Ile Val Leu Lys Lys Trp Tyr Thr Ile Phe Lys Asp His Val Ser
1 5 10 15
Leu Gly Asp Tyr Glu Ile His Asp Gly Met Asn Leu Glu Leu Tyr Tyr
20 25 30

Gln

50

A

<210> 19
<211> 73
<212> PRT
<213> Unknown Organism

<220>
<223> Description of Unknown Organism: Amino acid sequence for beacon from unknown organism

<400> 19
Met Ile Glu Val Val Cys Asn Asp Arg Leu Gly Lys Lys Val Arg Val
1 5 10 15
Lys Cys Asn Thr Asp Asp Thr Ile Gly Asp Leu Lys Lys Leu Ile Ala
20 25 30
Ala Gln Thr Gly Thr Arg Trp Asn Lys Ile Val Leu Lys Lys Trp Tyr
35 40 45
Thr Ile Phe Lys Asp His Val Ser Leu Gly Asp Tyr Glu Ile His Asp
50 55 60
Gly Met Asn Leu Glu Leu Tyr Tyr Gln
65 70

<210> 20
<211> 73
<212> PRT
<213> Homo sapiens

<400> 20
Met Ile Glu Val Val Cys Asn Asp Arg Leu Gly Lys Lys Val Arg Val
1 5 10 15
Lys Cys Asn Thr Asp Asp Thr Ile Gly Asp Leu Lys Lys Leu Ile Ala
20 25 30
Ala Gln Thr Gly Thr Arg Trp Asn Lys Ile Val Leu Lys Lys Trp Tyr
35 40 45
Thr Ile Phe Lys Asp His Val Ser Leu Gly Asp Tyr Glu Ile His Asp
50 55 60
Gly Met Asn Leu Glu Leu Tyr Tyr Gln
65 70

<210> 21
<211> 73
<212> PRT
<213> Murine sp.

57

A

<400> 21

Met	Ile	Glu	Val	Val	Cys	Asn	Asp	Arg	Leu	Gly	Lys	Lys	Val	Arg	Val
1				5					10				15		

Lys	Cys	Asn	Thr	Asp	Asp	Thr	Ile	Gly	Asp	Leu	Lys	Lys	Leu	Ile	Ala
			20					25					30		

Ala	Gln	Thr	Gly	Thr	Arg	Trp	Asn	Lys	Ile	Val	Leu	Lys	Lys	Trp	Tyr
				35				40				45			

Thr	Ile	Phe	Lys	Asp	His	Val	Ser	Leu	Gly	Asp	Tyr	Glu	Ile	His	Asp
			50			55				60					

Gly	Met	Asn	Leu	Glu	Leu	Tyr	Tyr	Gln							
			65		70										

<210> 22

<211> 73

<212> PRT

<213> Caenorhabditis elegans

<400> 22

Met	Ile	Glu	Ile	Thr	Val	Asn	Asp	Arg	Leu	Gly	Lys	Lys	Val	Arg	Ile
1				5					10				15		

Lys	Cys	Asn	Pro	Ser	Asp	Thr	Ile	Gly	Asp	Leu	Lys	Lys	Leu	Ile	Ala
			20				25				30				

Ala	Gln	Thr	Gly	Thr	Arg	Trp	Glu	Lys	Ile	Val	Leu	Lys	Lys	Trp	Tyr
			35			40		45							

Thr	Ile	Tyr	Lys	Asp	His	Ile	Thr	Leu	Met	Asp	Tyr	Glu	Ile	His	Glu
			50			55			60						

Gly	Phe	Asn	Phe	Glu	Leu	Tyr	Tyr	Gln							
			65		70										

<210> 23

<211> 66

<212> PRT

<213> Fasiola hepatica

<400> 23

Asp	Arg	Leu	Gly	Lys	Lys	Val	Arg	Val	Lys	Cys	Asn	Pro	Thr	Asp	Lys
1				5				10				15			

Val	Gly	Asp	Leu	Lys	Lys	Leu	Ile	Ala	Ala	Gln	Thr	Gly	Thr	Ala	Pro
			20			25				30					

Glu	Arg	Ile	Val	Leu	Lys	Lys	Trp	Tyr	Thr	Ile	Tyr	Lys	Asp	His	Val
			35			40		45							

Thr	Leu	Arg	Asp	Tyr	Glu	Ile	Asn	Asp	Gly	Met	Asn	Leu	Glu	Leu	Tyr
			50			55			60						

58

A

Tyr Gln
65

<210> 24
<211> 73
<212> PRT
<213> Oryza sativa

<400> 24
Met Ile Glu Val Val Cys Asn Asp Arg Leu Gly Lys Lys Val Arg Val
1 5 10 15

Lys Cys Asn Thr Asp Asp Thr Ile Gly Asp Leu Lys Lys Leu Ile Ala
20 25 30

Ala Gln Thr Gly Thr Arg Trp Asn Lys Ile Val Leu Lys Lys Trp Tyr
35 40 45

Thr Ile Tyr Lys Asp His Ile Thr Leu Ala Asp Tyr Glu Ile His Asp
50 55 60

Gly Met Gly Leu Glu Leu Tyr Tyr Asn
65 70

<210> 25
<211> 73
<212> PRT
<213> Saccharomyces cerevisiae

<400> 25
Met Ile Glu Val Val Cys Asn Asp Arg Leu Gly Lys Lys Val Arg Val
1 5 10 15

Lys Cys Asn Thr Asp Asp Thr Ile Gly Asp Leu Lys Lys Leu Ile Ala
20 25 30

Ala Gln Thr Gly Thr Arg Trp Asn Lys Ile Val Leu Lys Lys Trp Tyr
35 40 45

Thr Ile Leu Lys Asp His Ile Cys Leu Glu Asp Tyr Glu Val His Asp
50 55 60

Gln Thr Asn Leu Glu Leu Tyr Tyr Leu
65 70

<210> 26
<211> 76
<212> PRT
<213> Homo sapiens

<400> 26
Met Gln Ile Phe Val Lys Thr Leu Thr Gly Lys Thr Ile Thr Leu Glu
1 5 10 15

59

H

Val Glu Pro Ser Asp Thr Ile Glu Asn Val Lys Ala Lys Ile Gln Asp
20 25 30

Lys Glu Gly Ile Pro Pro Asp Gln Gln Arg Leu Ile Phe Ala Gly Lys
35 40 45

Gln Leu Glu Asp Gly Arg Thr Leu Ser Asp Tyr Asn Ile Gln Lys Glu
50 55 60

Ser Thr Leu His Leu Val Leu Arg Leu Arg Gly Gly
65 70 75

<210> 27

<211> 60

<212> PRT

<213> Arabidopsis thaliana

<400> 27

Gly Lys Thr Ile Ile Leu Glu Val Glu Ser Ser Asp Thr Ile Ala Asn
1 5 10 15

Val Lys Glu Lys Ile Gln Val Lys Glu Gly Ile Lys Pro Asp Gln Gln
20 25 30

Met Leu Ile Phe Phe Gly Gln Gln Leu Glu Asp Gly Val Thr Leu Gly
35 40 45

Asp Tyr Asp Ile His Lys Lys Ser Thr Leu Tyr Leu
50 55 60

60

A